

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Reed, Guy
Clement, Christophe Y.
- (ii) TITLE OF THE INVENTION: NOVEL PLATELET ACTIVATION PROTEIN
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson P.C.
(B) STREET: 225 Franklin Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110-2804
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 04-OCT-1996
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/005,074
(B) FILING DATE: 06-OCT-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Fraser, Janis K
(B) REGISTRATION NUMBER: 34,819
(C) REFERENCE/DOCKET NUMBER: 05433/020001
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-542-5070
(B) TELEFAX: 617-542-8906
(C) TELEX: 200154
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1373 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...1321
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCGAGAGGGC CAGAGGAGAA AGAGAGAGCG CGAAAGAGAG AGG ATG TCT CTC TCA 55
Met Ser Leu Ser
1

GAC TGG CAC CTG GCG GTG AAG CTG GCT GAC CAG CCA CTT ACT CCA AAG 103
Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys
5 10 15 20

TCT ATT CTT CGG TTG CCA GAG ACA GAA CTG GGA GAA TAC TCG CTA GGG 151
Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly
25 30 35

GGC TAT AGT ATT TCA TTT CTG AAG CAG CTT ATT GCT GGC AAA CTC CAG 199
Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln
40 45 50

GAG TCT GTT CCA GAC CCT GAG CTG ATT GAT CTG ATC TAC TGT GGT CGG 247
Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg
55 60 65

AAG CTA AAA GAT GAC CAG ACA CTT GAC TTC TAT GGC ATT CAA CCT GGG 295
Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly
70 75 80

TCC ACT GTC CAT GTT CTG CGA AAG TCC TGG CCT GAA CCT GAT CAG AAA 343
Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys
85 90 95 100

CCG GAA CCT GTG GAC AAA GTG GCT GCC ATG AGA GAG TTC CGG GTG TTG 391
Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu
105 110 115

CAC ACT GCC CTG CAC AGC AGC TCC TCT TAC AGG GAG GCG GTC TTT AAG 439
His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys
120 125 130

ATG CTC AGC AAT AAG GAG TCT CTG GAT CAG ATC ATT GTG GCC ACC CCA 487
Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro
135 140 145

GGC CTC AGC AGT GAC CCT ATT GCT CTT GGG GTT CTC CAG GAC AAG GAC 535
Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp
150 155 160

CTC TTC TCT GTC TTC GCT GAT CCC AAT ATG CTT GAT ACG TTG GTG CCT 583
Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro
165 170 175 180

GCT CAC CCA GCC CTC GTC AAT GCC ATT GTC CTG GTT CTG CAC TCC GTA Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val 185 190 195	631
GCA GGC AGT GCC CCA ATG CCT GGG ACT GAC TCC TCT TCC CGG AGC ATG Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met 200 205 210	679
CCC TCC AGC TCA TAC CGG GAT ATG CCA GGT GGC TTC CTG TTT GAA GGG Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly 215 220 225	727
CTC TCA GAT GAT GAG GAT GAC TTT CAC CCA AAC ACC AGG TCC ACA CCC Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro 230 235 240	775
TCT AGC AGT ACT CCC AGC TCC CGC CCA GCC TCC CTG GGG TAC AGT GGA Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly 245 250 255 260	823
GCT GCT GGG CCC CGG CCC ATC ACC CAG AGT GAG CTG GCC ACC GCC TTG Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu 265 270 275	871
GCC CTG GCC AGC ACT CCG GAG AGC AGC TCT CAC ACA CCG ACT CCT GGC Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly 280 285 290	919
ACC CAG GGT CAT TCC TCA GGG ACC TCA CCA ATG TCC TCT GGT GTC CAG Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln 295 300 305	967
TCA GGG ACG CCC ATC ACC AAT GAT CTC TTC AGC CAA GCC CTA CAG CAT Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His 310 315 320	1015
GCC CTT CAG GCC TCT GGG CAG CCC AGC CTT CAG AGC CAG TGG CAG CCC Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro 325 330 335 340	1063
CAG CTG CAG CAG CTA CGT GAC ATG GGC ATC CAG GAC GAT GAG CTG AGC Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser 345 350 355	1111
CTG CGG CCC TGC AGG CCA CCG GTG GGG ACA TCC AAG CAG CCC TGG AGC Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys Gln Pro Trp Ser 360 365 370	1159
TCA TCT TTG CTG GAG GAG CCC CAT GAA CTC CCT GCT TCC CCT GAA CCC Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala Ser Pro Glu Pro 375 380 385	1207
CCA GCA AGT TGC AGA GGC TAC TGC CCT TGG GAG GCA CTC ATG AAG GTG Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala Leu Met Lys Val 390 395 400	1255

CCT CCA TCT CTC CCT TCC CCA ATA TAC CTG ATG GTC AAC TCT AAA AAA 1303
 Pro Pro Ser Leu Pro Ser Pro Ile Tyr Leu Met Val Asn Ser Lys Lys
 405 410 415 420

AAA AAA AAA AAA AAA AAA TGAAATACCA CTACTCTGAT CGTTTTTTTCA CTGACCCG 1359
 Lys Lys Lys Lys Lys Lys
 425

GTGAGGCGGC GCGA
 1373

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Leu Ser Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro
 1 5 10 15
 Leu Thr Pro Lys Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu
 20 25 30
 Tyr Ser Leu Gly Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala
 35 40 45
 Gly Lys Leu Gln Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile
 50 55 60
 Tyr Cys Gly Arg Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly
 65 70 75 80
 Ile Gln Pro Gly Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu
 85 90 95
 Pro Asp Gln Lys Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu
 100 105 110
 Phe Arg Val Leu His Thr Ala Leu His Ser Ser Ser Tyr Arg Glu
 115 120 125
 Ala Val Phe Lys Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile
 130 135 140
 Val Ala Thr Pro Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu
 145 150 155 160
 Gln Asp Lys Asp Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp
 165 170 175
 Thr Leu Val Pro Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val
 180 185 190
 Leu His Ser Val Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser
 195 200 205
 Ser Arg Ser Met Pro Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe
 210 215 220
 Leu Phe Glu Gly Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr
 225 230 235 240
 Arg Ser Thr Pro Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu
 245 250 255
 Gly Tyr Ser Gly Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu
 260 265 270

Ala Thr Ala Leu Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr
 275 280 285
 Pro Thr Pro Gly Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser
 290 295 300
 Ser Gly Val Gln Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln
 305 310 315 320
 Ala Leu Gln His Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser
 325 330 335
 Gln Trp Gln Pro Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp
 340 345 350
 Asp Glu Leu Ser Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys
 355 360 365
 Gln Pro Trp Ser Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala
 370 375 380
 Ser Pro Glu Pro Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala
 385 390 395 400
 Leu Met Lys Val Pro Pro Ser Leu Pro Ser Pro Ile Tyr Leu Met Val
 405 410 415
 Asn Ser Lys Lys Lys Lys Lys Lys Lys Lys
 420 425

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 44...1273
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCGAGAGGGC CAGAGGAGAA AGAGAGAGCG CGAAAGAGAG AGG	ATG TCT CTC TCA	55
	Met Ser Leu Ser	
	1	
GAC TGG CAC CTG GCG GTG AAG CTG GCT GAC CAG CCA CTT ACT CCA AAG		103
Asp Trp His Leu Ala Val Lys Leu Ala Asp Gln Pro Leu Thr Pro Lys		
5 10 15 20		
TCT ATT CTT CGG TTG CCA GAG ACA GAA CTG GGA GAA TAC TCG CTA GGG		151
Ser Ile Leu Arg Leu Pro Glu Thr Glu Leu Gly Glu Tyr Ser Leu Gly		
25 30 35		
GGC TAT AGT ATT TCA TTT CTG AAG CAG CTT ATT GCT GGC AAA CTC CAG		199
Gly Tyr Ser Ile Ser Phe Leu Lys Gln Leu Ile Ala Gly Lys Leu Gln		
40 45 50		
GAG TCT GTT CCA GAC CCT GAG CTG ATT GAT CTG ATC TAC TGT GGT CGG		247
Glu Ser Val Pro Asp Pro Glu Leu Ile Asp Leu Ile Tyr Cys Gly Arg		
55 60 65		

AAG CTA AAA GAT GAC CAG ACA CTT GAC TTC TAT GGC ATT CAA CCT GGG Lys Leu Lys Asp Asp Gln Thr Leu Asp Phe Tyr Gly Ile Gln Pro Gly 70 75 80	295
TCC ACT GTC CAT GTT CTG CGA AAG TCC TGG CCT GAA CCT GAT CAG AAA Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu Pro Asp Gln Lys 85 90 95 100	343
CCG GAA CCT GTG GAC AAA GTG GCT GCC ATG AGA GAG TTC CGG GTG TTG Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu Phe Arg Val Leu 105 110 115	391
CAC ACT GCC CTG CAC AGC AGC TCC TCT TAC AGG GAG GCG GTC TTT AAG His Thr Ala Leu His Ser Ser Ser Ser Tyr Arg Glu Ala Val Phe Lys 120 125 130	439
ATG CTC AGC AAT AAG GAG TCT CTG GAT CAG ATC ATT GTG GCC ACC CCA Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile Val Ala Thr Pro 135 140 145	487
GGC CTC AGC AGT GAC CCT ATT GCT CTT GGG GTT CTC CAG GAC AAG GAC Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu Gln Asp Lys Asp 150 155 160	535
CTC TTC TCT GTC TTC GCT GAT CCC AAT ATG CTT GAT ACG TTG GTG CCT Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp Thr Leu Val Pro 165 170 175 180	583
GCT CAC CCA GCC CTC GTC AAT GCC ATT GTC CTG GTT CTG CAC TCC GTA Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val Leu His Ser Val 185 190 195	631
GCA GGC AGT GCC CCA ATG CCT GGG ACT GAC TCC TCT TCC CGG AGC ATG Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser Ser Arg Ser Met 200 205 210	679
CCC TCC AGC TCA TAC CGG GAT ATG CCA GGT GGC TTC CTG TTT GAA GGG Pro Ser Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe Leu Phe Glu Gly 215 220 225	727
CTC TCA GAT GAT GAG GAT GAC TTT CAC CCA AAC ACC AGG TCC ACA CCC Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr Arg Ser Thr Pro 230 235 240	775
TCT AGC AGT ACT CCC AGC TCC CGC CCA GCC TCC CTG GGG TAC AGT GGA Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu Gly Tyr Ser Gly 245 250 255 260	823
GCT GCT GGG CCC CGG CCC ATC ACC CAG AGT GAG CTG GCC ACC GCC TTG Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu Ala Thr Ala Leu 265 270 275	871
GCC CTG GCC AGC ACT CCG GAG AGC AGC TCT CAC ACA CCG ACT CCT GGC Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr Pro Thr Pro Gly 280 285 290	919

ACC CAG GGT CAT TCC TCA GGG ACC TCA CCA ATG TCC TCT GGT GTC CAG Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser Ser Gly Val Gln 295 300 305	967
TCA GGG ACG CCC ATC ACC AAT GAT CTC TTC AGC CAA GCC CTA CAG CAT Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln Ala Leu Gln His 310 315 320	1015
GCC CTT CAG GCC TCT GGG CAG CCC AGC CTT CAG AGC CAG TGG CAG CCC Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser Gln Trp Gln Pro 325 330 335 340	1063
CAG CTG CAG CAG CTA CGT GAC ATG GGC ATC CAG GAC GAT GAG CTG AGC Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp Asp Glu Leu Ser 345 350 355	1111
CTG CGG CCC TGC AGG CCA CCG GTG GGG ACA TCC AAG CAG CCC TGG AGC Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys Gln Pro Trp Ser 360 365 370	1159
TCA TCT TTG CTG GAG GAG CCC CAT GAA CTC CCT GCT TCC CCT GAA CCC Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala Ser Pro Glu Pro 375 380 385	1207
CCA GCA AGT TGC AGA GGC TAC TGC CCT TGG GAG GCA CTC ATG AAG GTG Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala Leu Met Lys Val 390 395 400	1255
CCT CCA TCT CTC CCT GTC 1273 Pro Pro Ser Leu Pro Val 405 410	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Leu	Ser	Asp	Trp	His	Leu	Ala	Val	Lys	Leu	Ala	Asp	Gln	Pro
1				5					10					15	
Leu	Thr	Pro	Lys	Ser	Ile	Leu	Arg	Leu	Pro	Glu	Thr	Glu	Leu	Gly	Glu
		20						25					30		
Tyr	Ser	Leu	Gly	Gly	Tyr	Ser	Ile	Ser	Phe	Leu	Lys	Gln	Leu	Ile	Ala
		35					40					45			
Gly	Lys	Leu	Gln	Glu	Ser	Val	Pro	Asp	Pro	Glu	Leu	Ile	Asp	Leu	Ile
	50					55				60					
Tyr	Cys	Gly	Arg	Lys	Leu	Lys	Asp	Asp	Gln	Thr	Leu	Asp	Phe	Tyr	Gly
65					70					75					80

Ile Gln Pro Gly Ser Thr Val His Val Leu Arg Lys Ser Trp Pro Glu
 85 90 95
 Pro Asp Gln Lys Pro Glu Pro Val Asp Lys Val Ala Ala Met Arg Glu
 100 105 110
 Phe Arg Val Leu His Thr Ala Leu His Ser Ser Ser Tyr Arg Glu
 115 120 125
 Ala Val Phe Lys Met Leu Ser Asn Lys Glu Ser Leu Asp Gln Ile Ile
 130 135 140
 Val Ala Thr Pro Gly Leu Ser Ser Asp Pro Ile Ala Leu Gly Val Leu
 145 150 155
 Gln Asp Lys Asp Leu Phe Ser Val Phe Ala Asp Pro Asn Met Leu Asp
 165 170 175
 Thr Leu Val Pro Ala His Pro Ala Leu Val Asn Ala Ile Val Leu Val
 180 185 190
 Leu His Ser Val Ala Gly Ser Ala Pro Met Pro Gly Thr Asp Ser Ser
 195 200 205
 Ser Arg Ser Met Pro Ser Ser Tyr Arg Asp Met Pro Gly Gly Phe
 210 215 220
 Leu Phe Glu Gly Leu Ser Asp Asp Glu Asp Asp Phe His Pro Asn Thr
 225 230 235 240
 Arg Ser Thr Pro Ser Ser Ser Thr Pro Ser Ser Arg Pro Ala Ser Leu
 245 250 255
 Gly Tyr Ser Gly Ala Ala Gly Pro Arg Pro Ile Thr Gln Ser Glu Leu
 260 265 270
 Ala Thr Ala Leu Ala Leu Ala Ser Thr Pro Glu Ser Ser Ser His Thr
 275 280 285
 Pro Thr Pro Gly Thr Gln Gly His Ser Ser Gly Thr Ser Pro Met Ser
 290 295 300
 Ser Gly Val Gln Ser Gly Thr Pro Ile Thr Asn Asp Leu Phe Ser Gln
 305 310 315 320
 Ala Leu Gln His Ala Leu Gln Ala Ser Gly Gln Pro Ser Leu Gln Ser
 325 330 335
 Gln Trp Gln Pro Gln Leu Gln Gln Leu Arg Asp Met Gly Ile Gln Asp
 340 345 350
 Asp Glu Leu Ser Leu Arg Pro Cys Arg Pro Pro Val Gly Thr Ser Lys
 355 360 365
 Gln Pro Trp Ser Ser Ser Leu Leu Glu Glu Pro His Glu Leu Pro Ala
 370 375 380
 Ser Pro Glu Pro Pro Ala Ser Cys Arg Gly Tyr Cys Pro Trp Glu Ala
 385 390 395 400
 Leu Met Lys Val Pro Pro Ser Leu Pro Val
 405 410

We claim: